

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using SW model

Run on: March 18, 2005, 14:31:06 ; Search time 420 Seconds  
(without alignments)  
6321.756 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atggtgacatgcgtcgtgc.....ttccaacgtgacatcgc 446

## Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCR\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCRUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	209.4	47.0	529 15 US-10-178-449A-48	Sequence 48, Appl
2	203	45.5	579 15 US-10-178-449A-31	Sequence 31, Appl
3	168.6	37.8	460 15 US-10-178-449A-3	Sequence 3, Appl
4	168.6	37.8	503 15 US-10-178-449A-1	Sequence 1, Appl
5	161	36.1	457 15 US-10-178-449A-46	Sequence 46, Appl
6	156.4	35.1	457 15 US-10-178-449A-13	Sequence 13, Appl
7	156.4	35.1	463 15 US-10-178-449A-9	Sequence 9, Appl
8	156.4	35.1	603 15 US-10-178-449A-11	Sequence 11, Appl
9	154.8	34.7	458 15 US-10-178-449A-21	Sequence 21, Appl
10	154.8	34.7	460 15 US-10-178-449A-17	Sequence 17, Appl
11	154.2	34.6	565 17 US-10-636-026-6	Sequence 6, Appl

12	154.2	34.6	565 18 US-10-636-026-6	Sequence 6, Appl
13	153.2	34.3	464 15 US-10-178-449A-19	Sequence 19, Appl
14	153.2	34.3	472 15 US-10-178-449A-23	Sequence 23, Appl
15	138.4	31.0	439 15 US-10-178-449A-15	Sequence 15, Appl
16	99.4	22.3	150 9 US-09-759-584-31	Sequence 31, Appl
17	91.4	20.5	150 9 US-09-759-584-33	Sequence 33, Appl
18	88.2	19.8	610 15 US-10-178-449A-29	Sequence 29, Appl
19	88.2	19.8	658 15 US-10-178-449A-7	Sequence 7, Appl
20	87.8	19.7	156 15 US-10-178-449A-34	Sequence 34, Appl
21	86.6	19.4	150 9 US-09-759-584-34	Sequence 34, Appl
22	85.8	19.2	501 15 US-10-178-449A-5	Sequence 5, Appl
23	74.8	16.8	250 15 US-10-178-449A-36	Sequence 36, Appl
24	65.8	14.8	333 9 US-09-770-696-283	Sequence 283, Appl
25	58.4	13.1	147 9 US-09-759-584-36	Sequence 36, Appl
26	56.6	12.7	470 14 US-10-178-213-88	Sequence 88, Appl
27	47.8	10.7	499 15 US-10-178-449A-25	Sequence 25, Appl
28	47.8	10.7	517 15 US-10-178-449A-27	Sequence 27, Appl
29	44.6	10.0	270 9 US-09-829-381A-14	Sequence 14, Appl
30	44.6	10.0	270 17 US-10-681-972-14	Sequence 14, Appl
31	44.6	10.0	286 9 US-09-829-381A-12	Sequence 12, Appl
32	44.6	10.0	286 17 US-10-681-972-12	Sequence 12, Appl
33	41.6	9.3	1616 9 US-09-732-561-21	Sequence 21, Appl
34	41.2	9.2	400 9 US-09-732-561-15	Sequence 15, Appl
35	40.8	9.1	500 9 US-09-829-381A-9	Sequence 9, Appl
36	40.8	9.1	500 17 US-10-681-972-9	Sequence 9, Appl
37	40.2	9.0	243 9 US-09-938-842A-2046	Sequence 2046, Appl
38	40.2	9.0	243 11 US-09-938-842A-2046	Sequence 2046, Appl
39	40.2	9.0	414 9 US-09-759-584-48	Sequence 48, Appl
40	40	9.0	414 13 US-10-006-252A-19	Sequence 19, Appl
41	40	9.0	414 17 US-10-388-361A-45	Sequence 45, Appl
42	39.6	8.9	335913 10 US-09-754-853A-2	Sequence 2, Appl
43	39.6	8.9	335913 10 US-09-754-853A-3	Sequence 3, Appl
44	39.2	8.8	3673778 16 US-10-312-841-1	Sequence 1, Appl
45	39	8.7	288 9 US-09-759-584-58	Sequence 58, Appl

## ALIGNMENTS

RESULT 1

US-10-178-449A-48

Sequence 48, Application US/10178449A

Publication No. US20030140368A1

GENERAL INFORMATION:

APPLICANT: Hermann, Omolayo O.

APPLICANT: Hermann, Rafael

APPLICANT: Lu, Albert L.

APPLICANT: McCutchen, Billy Fred

APPLICANT: Miao, Guo-Rua

APPLICANT: Presnail, James K.

APPLICANT: Rafaleki, Jan Antoni

APPLICANT: Meng, Zude

TITLE OF INVENTION: Plant Defensins

FILE REFERENCE: 35718/249123

CURRENT APPLICATION NUMBER: US/10/178, 449A

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 10/030, 516

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: PCT/US00/11952

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: US 60/133, 039

PRIOR FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 48

LENGTH: 529

TYPE: DNA

ORGANISM: Vernonia mespilifolia

FEATURE:

NAME/KEY: misc-feature

LOCATION: 480-515, 521, 529

OTHER INFORMATION: n = A,T,C or G

FEATURE:

NAME/KEY: CDS  
LOCATION: (25) ... (372)  
US-10-178-449A-48

Query Match 47.0%; Score 209.4; DB 15; Length 529;  
Best Local Similarity 82.5%; Pred. No. 4.2e-48;  
Matches 24; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214  
DB 78 AGAATCTCGAGTGTGAGAGAGAGCTATGCGAAGAACTAGCAAGACATGTCAGGCAA 137  
QY 215 CTGTGGCAATACGGGACATTTGCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 138 CTGTGGCAACACAGACATTTGTATATCAAGTGAATCATGGAGGGTGGCCCATGG 197  
QY 275 AGCGTGCATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 334  
DB 198 AGCTTGTCATGTGTGTCGAGGAAACACATGTCTTTTGTATTCTCAATTGTAAAAAAGC 257  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAAACAATGCTGCAAGACAACTTAATGC 394  
DB 258 TGAAGAACTCGCTCAAGATTAAGTAAAGACAGAAAGCTTGCTTAAGACAACTCAAGGC 317  
QY 395 CCAAAAGCTTGACCGGTATGCGCAAGAAAGTGTCCAAAGCTTGAACATCC 445  
DB 318 AGATAGTTTGACCATGATGCAAAAGATGATCAAAATGTGCAACATCC 368

## RESULT 2

US-10-178-449A-31  
Sequence 31, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Presnail, James K.  
APPLICANT: Rafaleki, Jan antoni  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178, 449A  
PRIOR FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/133,039  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Vernonia mespilifolia  
US-10-178-449A-31

Query Match 45.5%; Score 203; DB 15; Length 579;  
Best Local Similarity 81.1%; Pred. No. 2.7e-46;  
Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214  
DB 92 AGAATCTCGAGTGTGAGAGAGAGCTATGCGAAGAACTAGCAAGACATGTCAGGCAA 151  
QY 215 CTGTGGCAATACGGGACATTTGCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 152 CTGTGGCAACACAGACATTTGTATATCAAGTGAATCATGGAGGGTGGCCCATGG 211  
QY 275 AGCGTGCATGTGTGCTAAGCGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAAGC 334

DB 212 AGCTTGTCATGTGCGGAGGAAACACATGTGCTTTTGTATTTCATTTGAAAAAAGC 271  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAATGC 394  
DB 272 TGAAGAACTCGCTCAAGATTAAGTTAAAGCTGAAGCTTGCAAAAGACAACTCAAGGC 331  
QY 395 CCAAAAGCTTGACCGGTATGCGCAAGAAAGTGTTCGAAAGCTTGAACATCC 445  
DB 332 AGATAGTTTGACCATGATGCAAAAGATGATCAAAATGTGCAACATCC 382

## RESULT 3

US-10-178-449A-3  
Sequence 3, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Presnail, James K.  
APPLICANT: Rafaleki, Jan antoni  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178, 449A  
PRIOR FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/133,039  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 460  
TYPE: DNA  
ORGANISM: Dimorphotheca sinuata  
US-10-178-449A-3

Query Match 37.8%; Score 168.6; DB 15; Length 460;  
Best Local Similarity 81.6%; Pred. No. 1e-36;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214  
DB 87 AGAATCGGACCTGTGAGAAAGTGTGAGAAAGCTAGCAAGACATGTCAGGCAA 146  
QY 215 CTGTGGCAATACGGGACATTTGTCACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 147 CTGTGGCAACACGGGACATGTCAGACCAAGTAAAGTGTGGAGACATGCAAGCCATGG 206  
QY 275 AGCGTGCATGTGTGCGTGAAGGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAAGC 334  
DB 207 TGGGTGTCATGTGCGGTGGGAAACACATGTGCTTCTGTTACTTCAATTGTAAAAAAGC 266  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAATG 393  
DB 267 CGAAAGCTTGCCCAAGACAACTTCAAGCTTCAAAATTCGCGGTGATGACGTTAAAG 325

## RESULT 4

US-10-178-449A-1  
Sequence 1, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred

```

; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafaleki, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Dimorphotheca sinuata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 321..349, 416, 458, 474, 479, 482, 502
; OTHER INFORMATION: n = A,T,C or G

```

```

Query Match      37.8%; Score 168.6; DB 15; Length 503;
Best Local Similarity 81.6%; Pred. No. 1,1e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

```

```

Qy      155 AGATATGCGATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214
Db      80 AGAATCGCGAGCTGTGAGAACTGTGAGAAAGCTAGCAAGACATGTCAGGCAA 139
Qy      215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGGAGGTCGCCCATGG 274
Db      140 CTGTGGCAACACGGGACACGTGTGACGACCACTGTAAAGTCGGGAGACTGCAAGCCCATGG 199
Qy      275 AGCGTGCATGTGCGTAACGGGAACACATGTGTTCTGTACTTCAATTGTAAAGAAC 334
Db      200 TGCGTGCATGTGCGTGTGTGGAAACACATGTCTTCTGCTACTTCAATTGTAAAGAAC 259
Qy      335 CGAAAGCTTGCTCAGACAAACTTAAAGCCGAACAACTCGCTCAGACAAACTTAAAG 393
Db      260 CGAAAGCTTGCTCAGACAAACTTAAAGCGTGAAGAAATTCGGCGGTATGACGTTAAAG 318

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## RESULT 5

```

US-10-178-449A-46
; Sequence 46, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafaleki, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46

```

```

; LENGTH: 461
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14) ... (340)
; US-10-178-449A-46

```

```

Query Match      36.1%; Score 161; DB 15; Length 461;
Best Local Similarity 77.9%; Pred. No. 1,4e-34;
Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

```

```

Qy      155 AGATATGCGATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214
Db      76 AGAATCGATCGGTGAGAGGAAATATGTGAGAAAGCAAGACATGTCGGGAAA 135
Qy      215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGGAGGTCGCCCATGG 274
Db      136 ATGTGGCAACACAGAACACTGTGACGACAGTGCMACTTGGAGGGTGCAGCCCATGG 195
Qy      275 AGCGTGCATGTGCGTAACGGGAACACATGTGTTCTGTACTTCAATTGTAAAGAAC 334
Db      196 AGCTTGCACTGTCGCCGTGGGAACACATGTCTTCTGCTACTTCAACTGTTCCAAAGC 255
Qy      335 CGAAAGCTTGCTCAGACAAACTTAAAGCCGAACAACTCGCTCAGACAAACTTAAAGC 394
Db      256 CGAAGAGTGGCTCAGATTAACCTCATAGCAAGAAAGCTCGCCAAAGAAATTGAAGC 315
Qy      395 CGAAAGCT 403
Db      316 CGAAAGGT 324

```

## RESULT 6

```

US-10-178-449A-13
; Sequence 13, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafaleki, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 424..436
; OTHER INFORMATION: n = A,T,C or G
; US-10-178-449A-13

```

```

Query Match      35.1%; Score 156.4; DB 15; Length 457;
Best Local Similarity 77.2%; Pred. No. 2.6e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

```

```

Qy      155 AGATATGCGATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214

```

```
Db      91 AGAATCGATCGGTGAAGGAGCACTATGTGAGAGGCAAGCAATGTTGAAA 150
Qy      215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAAATGAGGAGGTGGCCCATGG 274
Db      151 TTGTGTAAACAAGACATTGTGACGACCAATGCAAGCTTGGAGGGTGCAGCCCATGG 210
Qy      275 AGCGTGCATGTGGGTGAACGGGAAACATGTCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      211 AGCTTGTCATGTGGCGGTGGGAAACATGTGCTTGTCTACTTCCAGTGCCCAAGC 270
Qy      335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAAACAATGCTCAAGCAAACTTAATGC 394
Db      271 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCCAAAGAGAAATTGAAGC 330
Qy      395 CCAAAA 400
Db      331 TGAATA 336
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```
RESULT 7
US-10-178-449A-9
; Sequence 9, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 413
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-9
```

```
Query Match      35.1%; Score 156.4; DB 15; Length 463;
Best Local Similarity 77.2%; Pred. No. 2.7e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      155 AGATATCGATCCGTTAGTGAAGACTATGCGAAGAGTAGCAAGACATGTGCGGAAA 214
Db      94 AGAAATCGATCGGTGAAGGAGCACTATGTGAGAGGCAAGCAATGTGTGAAA 153
Qy      215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAAATCATGGAGGGTGGCCCATGG 274
Db      154 TTGTGTAAACAAGACATTGTGACGACCAATGCAAGCTTGGAGGGTGCAGCCCATGG 213
Qy      275 AGCGTGCATGTGGGTGAACGGGAAACATGTCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      211 AGCTTGTCATGTGGCGGTGGGAAACATGTGCTTGTCTACTTCCAGTGCCCAAGC 273
Qy      335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAAACAATGCTCAAGCAAACTTAATGC 394
```

```
Db      274 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCCAAAGAGAAATTGAAGC 333
Qy      395 CCAAAA 400
Db      334 TGAATA 339
```

```
RESULT 8
US-10-178-449A-11
; Sequence 11, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
US-10-178-449A-11
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```
Query Match      35.1%; Score 156.4; DB 15; Length 603;
Best Local Similarity 77.2%; Pred. No. 3e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      155 AGATATCGATCCGTTAGTGAAGACTATGCGAAGAGTAGCAAGACATGTGCGGAAA 214
Db      101 AGAAATCGATCGGTGAAGGAGCACTATGTGAGAGGCAAGCAATGTGTGAAA 160
Qy      215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAAATCATGGAGGGTGGCCCATGG 274
Db      161 TTGTGTAAACAAGACATTGTGACGACCAATGCAAGCTTGGAGGGTGCAGCCCATGG 220
Qy      275 AGCGTGCATGTGGGTGAACGGGAAACATGTGCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      221 AGCTTGTCATGTGGCGGTGGGAAACATGTGCTTGTCTACTTCCAGTGCCCAAGC 280
Qy      335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAAACAATGCTCAAGCAAACTTAATGC 394
Db      281 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCCAAAGAGAAATTGAAGC 340
Qy      395 CCAAAA 400
Db      341 TGAATA 346

RESULT 9
US-10-178-449A-21
; Sequence 21, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
```

```
APPLICANT: Presnail, James K.
APPLICANT: Rafaleki, Jan antoni
APPLICANT: Weng, Zude
FILE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 458
TYPE: DNA
ORGANISM: Parthenium argentatum Grey
FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..375, 402..452
OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-21
```

```
Query Match          34.7%; Score 154.8; DB 15; Length 458;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCGATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGCTGGGAAA 214
DB 72 AGAAATCGATCGGTGGAAGGAGAACTATGTGAGAAAGCAAGACATGCTGGAAA 131
QY 215 CTGTGCGAATACGGGACATTTGTGCAACCATGTAATCATGGAGGGGTGGCCCATGG 274
DB 132 TTGTGTACACACAGACAGACATGTGACGACCAATGCAAGCTTTGGAGGGTGCAGCCATGG 191
QY 275 AGCGTGCATGTGGCTGAACGGGAAACATGTGTTTCTGTTACTTCAATTGTAAGAAAGC 334
DB 192 AGCTGTGATGTGGCGCGGTGGGAAACATGTGCTTCTGCTACTTCCAGTCCCAAGC 251
QY 335 CGAAAGCTTGCTCAGACAACTTAAGCCGAAACAATCGCTGCTAAGACAACTTAATGC 394
DB 252 CGAAGATGCGCCAGATTAATCTCCGAGCTGAGAGAGCTTCCCAAGGAAAGATTGAAGC 311
QY 395 CCAAAA 400
DB 312 TGA AAA 317
```

```
RESULT 10
US-10-178-449A-17
Sequence 17, Application US/10178449A
Publication No. US20030140368A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert L.
APPLICANT: McCutchen, Billy Fred
APPLICANT: Miao, Guo-Hua
APPLICANT: Presnail, James K.
APPLICANT: Rafaleki, Jan antoni
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
```

```
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 460
TYPE: DNA
ORGANISM: Parthenium argentatum Grey
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342
OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-17
```

```
Query Match          34.7%; Score 154.8; DB 15; Length 460;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCGATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGCTGGGAAA 214
DB 89 AGAAATCGATCGGTGGAAGGAGAACTATGTGAGAAAGCAAGACATGCTGGAAA 148
QY 215 CTGTGCGAATACGGGACATTTGTGCAACCATGTAATCATGGAGGGGTGGCCCATGG 274
DB 149 TTGTGTACACACAGACAGACATGTGACGACCAATGCAAGCTTTGGAGGGTGCAGCCATGG 208
QY 275 AGCGTGCATGTGCGTGAACGGGAAACATGTGTTTCTGTTACTTCAATTGTAAGAAAGC 334
DB 209 AGCTGTGATGTGGCGGTGGGAAACATGTGCTTCTGCTACTTCCAGTCCCAAGC 268
QY 335 CGAAAGCTTGCTCAGACAACTTAAGCCGAAACAATCGCTGCTAAGACAACTTAATGC 394
DB 269 CGAAGATGCGCCAGATTAATCTCCGAGCTGAGAGAGCTTCCCAAGGAAAGATTGAAGC 328
QY 395 CCAAAA 400
DB 329 TGA AAA 334
```

```
RESULT 11
US-10-636-396-6
Sequence 6, Application US/10636396
Publication No. US20040073971A1
GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jon
APPLICANT: Hu, Xu
APPLICANT: Lu, Guhua
TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
FILE REFERENCE: 5718-90
CURRENT APPLICATION NUMBER: US/10/636,396
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: US/09/589,733C
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 565
TYPE: DNA
ORGANISM: Helianthus annuus
US-10-636-396-6
```

```
Query Match          34.6%; Score 154.2; DB 17; Length 565;
Best Local Similarity 76.5%; Pred. No. 1.2e-32;
Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCGATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGCTGGGAAA 214
DB 99 AGAAATCGATCGGTGGAAGGAGAACTATGTGAGAAAGCAAGACATGCTGGAAAC 158
```



```
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 368
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-23
```

```
Query Match          34.3%; Score 153.2; DB 15; Length 472;
Best Local Similarity 76.4%; Pred. No. 2.1e-32;
Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCAATCCGTTAGTGGAAGAACTATGCGAAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 86 AGAAATCGATCGGTGGAAGGAGAACTATGTGAGAAAGCAAGACATGTCGGA 145
QY 215 CTGTGCAATACGGGACATTGTGCAACCAATGTAATCATGGAGGGTGGCCCATGG 274
DB 146 TTGTGTTAACACAAAGACATGTGACGACCAATGCAAGCTTGGAGGGTGGACCCATGG 205
QY 275 AGCGTTCATGTGCGTAAACGGGAACACATGTGTTCTGTACTTCAATGTAAAGAGC 334
DB 206 AGCTTGTCATGTGCGCGGTGGGAACACATGTGCTTCTGCTACTTCCAGTGCCCAAGC 265
QY 335 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACAACTGCTCAAGCAAACTTAATGC 394
DB 266 CGAGAAATGCGCCAGATTAACCTCGAGCTGAAGAGCTTGCCAAAGAGAAATTGAAGT 325
QY 395 CCAAAA 400
DB 326 TGA AAA 331
```

```
RESULT 15
US-10-178-449A-15
; Sequence 15, Application US/10/178,449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert T.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnall, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 439
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```
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 276,288,349,438
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-15
```

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Query Match          31.0%; Score 138.4; DB 15; Length 439;
Best Local Similarity 71.9%; Pred. No. 2.8e-28;
Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;
```

```
QY 155 AGATATGCAATCCGTTAGTGGAAGAACTATGCGAAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 93 AGAAATCGATCGGTGGAAGGAGAACTATGTGAGAAAGCAAGACATGTCGGA 152
QY 215 CTGTGCAATACGGGACATTGTGCAACCAATGTAATCATGGAGGGTGGCCCATGG 274
DB 153 TTGTGTTAACACAAAGACATTTGTGACGACCAATGCAAGCTTGGAGGGTGGACCCATGG 212
QY 275 AGCGTTCATGTGCGTAAACGGGAACACATGTGTTCTGTACTTCAATGTAAAGAGC 334
DB 213 AGCTTGTCATGTGCGCGGTGGGAACACATGTGCTTCTGCTACTTCCAGTGCCCAAGC 272
QY 335 CGAAAGCTTGCTCAA-GACAACTTAAAGCCGAACCACTGCTCAAGACAACTTAATG 393
DB 273 CGAAGATGCGCCAGATTAACCTCGAGCTGAAGAGCTTGCCAAAGAGAAATTGAA 332
QY 394 CCAAAAAGCTTGACCGTGAATGCCAAGA 420
DB 333 GCTGAAAAAGAGCCAGCAAACTTGA 359
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Search completed: March 18, 2005, 19:33:33
Job time : 422 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 06:45:35 ; Search time 388 Seconds  
(without alignments)  
6804.651 Million cell updates/sec

Title: US-09-763-019-5  
Perfect score: 446  
Sequence: 1 atggtgacgcgtgcgtgc.....ttccaacgtgacatcgcg 446

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*\n2: geneseqn1990s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001as:\*\n5: geneseqn2001bs:\*\n6: geneseqn2002as:\*\n7: geneseqn2002bs:\*\n8: geneseqn2003as:\*\n9: geneseqn2003bs:\*\n10: geneseqn2003cs:\*\n11: geneseqn2003ds:\*\n12: geneseqn2004as:\*\n13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	446	3	AA251379 Dahlia me
2	446	100.0	446	3	AA299323 DNA encod
3	287.2	64.4	606	3	AA299326 DNA encod
4	284	63.7	557	3	AA299336 DNA encod
5	215.2	48.3	534	3	AA251396 Portion o
6	215.2	48.3	534	3	AA299325 DNA encod
7	212	47.5	485	3	AA299335 DNA encod
8	209.4	47.0	529	11	ADM77231 Ironweed
9	203	45.5	579	11	ADM77214 Dahlia me
10	177.2	39.7	577	3	AA251378 Dahlia me
11	173.2	38.8	485	3	AA299333 DNA encod
12	172.2	38.6	446	3	AA299329 DNA encod
13	170	38.1	1093	3	AA299334 DNA encod
14	169.2	37.9	522	3	AA299324 DNA encod
15	168.6	37.8	460	5	AA251387 Plant def
16	168.6	37.8	460	11	ADM77186 African d
17	168.6	37.8	503	5	AA251386 Plant def
18	168.6	37.8	503	11	ADM77184 African d
19	167.2	37.5	534	3	AA299327 DNA encod
20	166	37.2	434	3	AA299332 DNA encod

21	166	37.2	437	3	AA299331 DNA encod
22	166	37.2	443	3	AA299330 DNA encod
23	166	37.2	488	3	AA299338 DNA encod
24	166	37.2	575	3	AA299339 DNA encod
25	165.6	37.1	316	3	AA251397 Portion o
26	165.6	37.1	316	3	AA299328 DNA of p
27	164	36.8	485	3	AA299337 DNA encod
28	161	36.1	461	11	ADM77229 Sunflower
29	157.8	35.4	523	3	AA251376 Dahlia me
30	156.4	35.1	457	5	AA254392 Plant def
31	156.4	35.1	457	11	ADM77186 Mexican r
32	156.4	35.1	463	5	AA254390 Plant def
33	156.4	35.1	463	11	ADM77192 Mexican r
34	156.4	35.1	603	5	AA254391 Plant def
35	156.4	35.1	603	11	ADM77194 Mexican r
36	154.8	34.7	458	5	AA254396 Plant def
37	154.8	34.7	458	11	ADM77204 Mexican r
38	154.8	34.7	460	5	AA254394 Plant def
39	154.8	34.7	460	11	ADM77200 Mexican r
40	154.2	34.6	565	5	AA254395 Plant def
41	153.2	34.3	464	5	AA254395 Plant def
42	153.2	34.3	464	11	ADM77202 Mexican r
43	153.2	34.3	472	5	AA254397 Plant def
44	153.2	34.3	472	11	ADM77206 Mexican r
45	146.8	32.9	399	3	AA251375 Dahlia me

## ALIGNMENTS

RESULT 1  
AA251379  
ID AA251379 standard; DNA; 446 BP.

XX AA251379;  
XX 06-JUN-2000 (first entry)  
XX Dahlia merckii antimicrobial protein Dm-AMPI gene.

XX Antimicrobial protein; Dm-AMPI; transgenic plant; microbial infection;  
XX Bacteria; Fungi; field crop; fruit; vegetable; canola; banana; sunflower;  
XX apple; ds.

XX Dahlia merckii.

XX Key Location/Qualifiers

FT CDS 1..446

FT /tag= a "Antimicrobial protein Dm-AMPI"

FT /note= "Does not include stop codon"

FT /partial

FT sig\_peptide 1..176

FT /tag= e

FT /note= "excludes intron"

FT exon 1..64

FT /tag= b

FT /number= 1

FT intron 65..156

FT /tag= c

FT /number= 1

FT exon 157..446

FT /tag= d

FT /number= 2

FT mat\_peptide 177..326

FT /tag= f

FT /product= "Mature Dm-AMPI protein"

FT misc\_feature 327..446

FT /tag= g

FT /note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"

FT ADm77184 African d

FT AA299327 DNA encod

FT AA299332 DNA encod

PN WO20001196-A1.

```

XX 02-MAR-2000.
XX 17-AUG-1999; 99WO-GB002720.
XX 18-AUG-1998; 98GB-00018003.
XX (ZENE ) ZENECA LTD.
XX Evans IU, Ray JA;
XX WPI: 2000-237658/20.
XX P-PSDB; AAY70315.
XX Polynucleotide sequences and expression products useful for producing
XX transgenic plants that are resistant to microbial infections.
XX Claim 1; Fig 1A; 77pp; English.
XX The present sequence is a Dahlia merckii cDNA encoding an antimicrobial
XX preprotein Dm-AMPI. This sequence is useful in the production of
XX transgenic plants which show improved resistance to infections by
XX microorganisms such as bacteria and fungi. Transgenic plants include e.g.
XX field crops, fruits and vegetables, such as canola, sunflower, tomato,
XX apple, banana, pear and mango
XX
SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;
Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGAATCGGTCGGTTCCTCCGCGTTCCTTCGATCCCTTTGCTGCGCCATC 60
DB 1 ATGGTGAATCGGTCGGTTCCTCCGCGTTCCTTCGATCCCTTTGCTGCGCCATC 60
QY 61 TCAGGTTATCAAACTTTAGTTCATTATGAAATAGATGATTTATTTCTTTATGG 120
DB 61 TCAGGTTATCAAACTTTAGTTCATTATGAAATAGATGATTTATTTCTTTATGG 120
QY 121 TTTTATGTGTTCTGCAAGTTCGCAATATGAGTAGATATCGATCCGTTAGTGAGAAC 180
DB 121 TTTTATGTGTTCTGCAAGTTCGCAATATGAGTAGATATCGATCCGTTAGTGAGAAC 180
QY 121 TTTTATGTGTTCTGCAAGTTCGCAATATGAGTAGATATCGATCCGTTAGTGAGAAC 180
DB 121 TTTTATGTGTTCTGCAAGTTCGCAATATGAGTAGATATCGATCCGTTAGTGAGAAC 180
QY 181 TATGCGAAGAAAGCTAGCAAGACATGTCGGGAAACCTGTGCAATACGGGACATTGTGACA 240
DB 181 TATGCGAAGAAAGCTAGCAAGACATGTCGGGAAACCTGTGCAATACGGGACATTGTGACA 240
QY 241 ACCAATGTAAATCATGGAGGGGTGCGGCCCATGGAGGTGCAATGTCGTAACGGGAAAC 300
DB 241 ACCAATGTAAATCATGGAGGGGTGCGGCCCATGGAGGTGCAATGTCGTAACGGGAAAC 300
QY 301 ACATGTTCTTCTGTTACTTCAATTTGTAATAAAAGCCGAAAGCTTGCTCAAGACAACTTA 360
DB 301 ACATGTTCTTCTGTTACTTCAATTTGTAATAAAAGCCGAAAGCTTGCTCAAGACAACTTA 360
QY 361 AAGCGCAACAACCTGCTCAAGACAACTTAATGCGCAAAAGCTTGACCGTGATGCCAAGA 420
DB 361 AAGCGCGAACAACCTGCTCAAGACAACTTAATGCGCAAAAGCTTGACCGTGATGCCAAGA 420
QY 421 AAGTGTTCCAAAAGCTGGAACATCCG 446
DB 421 AAGTGTTCCAAAAGCTGGAACATCCG 446
RESULT 2
ID AA299323 standard; DNA; 446 BP.
XX AA299323;
XX 03-JUL-2000 (first entry)

```

```

DE DNA encoding the Dahlia antimicrobial protein 1 (AMPI).
XX Antimicrobial protein; AMPI; transgenic plant; linker propeptide;
XX protein expression; ss.
XX
OS Dahlia merckii.
FH Key Location/Qualifiers
FT CDS 1..446
FT /tag= a
FT /note= "contains 1 intron; no termination codon"
FT exon 1..64
FT /tag= b
FT /number= 1
FT intron 65..156
FT /tag= c
FT /number= 1
FT exon 157..446
FT /tag= d
FT /number= 2
FT mat_peptide 177..314
FT /tag= e
PN W020001175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZENE ) ZENECA LTD.
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IU, Ray JA;
DR WPI: 2000-246564/21.
DR P-PSDB; AAY64050.
XX
PT Improving expression of polypeptides in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Example 1; Fig 1; 151pp; English.
XX
XX The present sequence encodes a Dahlia antimicrobial protein (AMP) 1. The
XX AMP1 protein is used to produce transgenic plants, using the method of
XX the invention. The specification describes methods for improving
XX expression levels of one or more proteins in a transgenic plant. The
XX method comprises inserting a DNA sequence having a promoter region
XX operably linked to two or more protein encoding regions separated by a
XX DNA sequence coding for a linker propeptide and a terminator region. The
XX method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;
Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGAATCGGTCGGTTCCTCCGCGTTCCTTCGATCCCTTTGCTGCGCCATC 60
DB 1 ATGGTGAATCGGTCGGTTCCTCCGCGTTCCTTCGATCCCTTTGCTGCGCCATC 60
QY 61 TCAGGTTATCAAACTTTAGTTCATTATGAAATAGATGATTTATTTCTTTATGG 120
DB 61 TCAGGTTATCAAACTTTAGTTCATTATGAAATAGATGATTTATTTCTTTATGG 120
QY 121 TTTTATGTGTTCTGCAAGTTCGCAATATGAGTAGATATCGATCCGTTAGTGAGAAC 180

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Db      121 TTTTATGTTCTGACAAAGTTGCAAAATATTAGATATCGATCCGTTAGTGAAGAC 180
Qy      181 TATGCGGAAGAGTCAGACAGATGTCGGGAAACCTGGCAATACGGGACATTGTGACA 240
Db      181 TATGCGGAAGAGTCAGACAGATGTCGGGAAACCTGGCAATACGGGACATTGTGACA 240
Qy      241 ACCAATGTAATCATGAGGAGGTGCGGCCCATGAGGCGTGCATGTCGTAAACGGGAAC 300
Db      241 ACCAATGTAATCATGAGGAGGTGCGGCCCATGAGGCGTGCATGTCGTAAACGGGAAC 300
Qy      301 ACATGTTCTTCTGTTACTTCAATTGTAAAGCCGAAAGCTTGCTCAAGACAACTTA 360
Db      301 ACATGTTCTTCTGTTACTTCAATTGTAAAGCCGAAAGCTTGCTCAAGACAACTTA 360
Qy      361 AAGCGCAACAACTGCGTCAAGACAACTTAATGCCCAAGCTTGACCGGTGATGCCAAGA 420
Db      361 AAGCGCAACAACTGCGTCAAGACAACTTAATGCCCAAGCTTGACCGGTGATGCCAAGA 420
Qy      421 AAGTGTTCCTCAACGTTGAACATCCG 446
Db      421 AAGTGTTCCTCAACGTTGAACATCCG 446

```

RESULT 3  
AAZ99326  
ID AAZ99326 standard; DNA; 606 BP.

XX AAZ99326;  
XX 03-JUL-2000 (first entry)  
XX DNA encoding a fusion protein of DmAMP1 and RaAFP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
XX protein expression; plant defensin; RaAFP2; antifungal protein; AFP2; ss.  
XX Synthetic.  
XX Dahlia merckii.  
XX Undentified.

XX Key Location/Qualifiers  
XX CDS 76..597  
XX FT /\*cag= a  
XX FT 160..309  
XX FT misc\_feature /\*cag= b  
XX FT /note= "encodes DmAMP1"  
XX FT misc\_feature 442..594  
XX FT /cag= C  
XX FT /note= "encodes RaAFP2"

XX PN WO200011175-A1.

XX PD 02-MAR-2000.

XX PF 17-AUG-1999; 99WO-GB002716.

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX PA (ZENE ) ZENECA LTD.

XX PI Broekert WF, Francois IEJA, De Bolle MFC, Evans IU, Ray JA;

XX DR WPI; 2000-246564/21.

XX DR P-PSDB; AAY84059.

XX PT Improving expression of polypeptides in plants involves coexpression of  
XX two or more proteins in plants within a single transcription unit.

XX PS Example 2; Fig 11; 15pp; English.

XX CC The present sequence encodes a protein of the invention, comprising the

CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker  
CC propeptide of the invention. The specification describes methods for  
CC improving expression levels of one or more proteins in a transgenic  
CC plant. The method comprises inserting a DNA sequence having a promoter  
CC region operably linked to two or more protein encoding regions separated  
CC by a DNA sequence coding for a linker propeptide and a terminator region.  
CC The method is used to produce proteins in plants. The linker propeptide  
CC comprising a cleavage site, whereby the expressed polypeptide is post-  
CC translationally processed into the component protein molecules. The  
CC propeptide sequence is rich in amino acids A, V, S and T and contains  
CC dipeptide sequences consisting of either two acidic, two basic or one  
CC acidic and one basic residue as a cleavable linker sequence  
XX

SO Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;  
Query Match 64.4%; Score 287.2; DB 3; Length 606;  
Best Local Similarity 99.0%; Pred. No. 6.1e-69;  
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy      155 AGATATGTCATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGATGTCGGGAAA 214
Db      138 AGATATGTCATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGATGTCGGGAAA 197
Qy      215 CTGTGGCAATACGCGACATTGTGACCAATGTAAATCATGCGAGGTCGCCCATGG 274
Db      198 CTGTGGCAATACGCGACATTGTGACCAATGTAAATCATGCGAGGTCGCCCATGG 257
Qy      275 AGCGTTCATGTGCGTGAACGGAACCATGTGTTCTGTACTTCAATTGTAAAGAGC 334
Db      258 AGCGTTCATGTGCGTGAACGGAACCATGTGTTCTGTACTTCAATTGTAAAGAGC 317
Qy      335 CGAAAGCTTGCTCAAGACAACTTAAGCCGAAACATGCTGCTCAAGACAACTTAATGC 394
Db      318 CGAAAGCTTGCTCAAGACAACTTAAGCCGAAACATGCTGCTCAAGACAACTTAATGC 377
Qy      395 CCAAAAGCTTGACCGGTGATGCCAAGAAAGTGTTCCAAGCTTGAAACATCCG 446
Db      378 CCAAAAGCTTGACCGGTGATGCCAAGAAAGTGTTCCAAGCTTGAAACATCCG 429

```

RESULT 4  
AAZ99336  
ID AAZ99336 standard; DNA; 557 BP.

XX AAZ99336;

XX 03-JUL-2000 (first entry)

XX DNA encoding a fusion protein of DmAMP1 and RaAFP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
XX protein expression; plant defensin; RaAFP2; antifungal protein; AFP2; ss.

XX Synthetic.  
XX Dahlia merckii.  
XX Undentified.

XX Key Location/Qualifiers  
XX CDS 3..548  
XX FT /\*cag= a  
XX FT /product= "fusion protein of DmAMP1 and RaAFP2"

XX PN WO200011175-A1.

XX PD 02-MAR-2000.

XX PF 17-AUG-1999; 99WO-GB002716.

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX PA (ZENE ) ZENECA LTD.

XX PT Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX WPI; 2000-246564/21.  
 DR P-PSDB; AAY64069.  
 XX  
 PT Improving expression of polypeptides in plants involves coexpression of  
 XX two or more proteins in plants within a single transcription unit.  
 XX  
 PS Disclosure; Fig 31; 151pp; English.  
 XX  
 CC The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RAFP2), linked by a linker  
 CC peptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker polypeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker polypeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC polypeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 CC  
 XX Sequence 557 BP; 164 A; 122 C; 143 G; 128 T; 0 U; 0 Other;  
 SQ  
 Query Match 63.7%; Score 284; DB 3; Length 557;  
 Best Local Similarity 98.3%; Pred. No. 4,56-68;  
 Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 155 AGATATCGATCCGTTAGTGAAGAACTATGCGAGAAAGCTAGCAAGCATGTCGGGAAA 214  
 DB 65 AGATATCGATCCGTTAGTGAAGAACTATGCGAGAAAGCTAGCAAGCATGTCGGGCAA 124  
 QY 215 CTGTGGCAATACCGGAACTGTGACACCAATGTAAATCATGGAGGTCGGCCCATGG 274  
 DB 125 CTGTGGCAATACCGGAACTGTGACACCAATGTAAATCATGGAGGTCGGCCCATGG 184  
 QY 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 334  
 DB 185 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 244  
 QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAAATGC 394  
 DB 245 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAAATGC 304  
 QY 395 CGAAAAGCTTGACCGGTATGCCAAGAAAGTGTCCCAAGCTGAATGAAATCCG 446  
 DB 305 CGAAAAGCTTGACCGGTATGCCAAGAAAGTGTCCCAAGCTGAATGAAATCCG 356  
 RESULT 5  
 AAZ51396  
 ID AAZ51396 standard; DNA; 534 BP.  
 XX  
 AC AAZ51396;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Portion of pFAJ106 encoding Dahlia merckii antimicrobial protein.  
 XX  
 KW Antimicrobial protein; DmAMP; transgenic plant; microbial infection;  
 KM bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;  
 XX apple; plant transformation vector; ds.  
 OS Dahlia merckii.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 76..525  
 FT /\*tag= a

FT  
 XX /product= "Antimicrobial protein"  
 PN MO20001196-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 17-AUG-1999; 99MO-GB002720.  
 XX  
 PR 18-AUG-1999; 98GB-00018003.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PT Evans IJ, Ray JA;  
 XX WPI; 2000-237658/20.  
 DR P-PSDB; AAY70323.  
 XX  
 PT Polynucleotide sequences and expression products useful for producing  
 XX transgenic plants that are resistant to microbial infections.  
 XX  
 PS Example 3; Fig 7; 77pp; English.  
 XX  
 CC The present sequence corresponds to the region between XhoI and SacI  
 CC sites of plant transformation vector pFAJ106, which encompass the coding  
 CC region for Dahlia merckii antimicrobial protein, Dm-AMP1. The vector is  
 CC useful in the production of transgenic plants which show improved  
 CC resistance to infections by microorganisms such as bacteria and fungi.  
 CC Transgenic plants include e.g. field crops, fruits and vegetables, such  
 CC as canola, sunflower, tomato, apple, banana, pear and mango  
 CC  
 XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;  
 SQ  
 Query Match 48.3%; Score 215.2; DB 3; Length 534;  
 Best Local Similarity 98.6%; Pred. No. 4e-49;  
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 155 AGATATCGATCCGTTAGTGAAGAACTATGCGAGAAAGCTAGCAAGCATGTCGGGAAA 214  
 DB 138 AGATATCGATCCGTTAGTGAAGAACTATGCGAGAAAGCTAGCAAGCATGTCGGGCAA 197  
 QY 215 CTGTGGCAATACCGGAACTGTGACACCAATGTAAATCATGGAGGTCGGCCCATGG 274  
 DB 198 CTGTGGCAATACCGGAACTGTGACACCAATGTAAATCATGGAGGTCGGCCCATGG 257  
 QY 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 334  
 DB 258 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 317  
 QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAAATGC 374  
 DB 318 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAAATGC 357  
 RESULT 6  
 AAZ99325  
 ID AAZ99325 standard; DNA; 534 BP.  
 XX  
 AC AAZ99325;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1 and RAFP2.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker polypeptide;  
 KM protein expression; plant defensin; RAFP2; antifungal protein; AFP2; ss.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 76..522  
 FT /\*tag= a

FT	misc_feature	160..309	
FT		/*tag= b	
FT		/note= "encodes DmAMP1"	
FT	misc_feature	370..538	
FT		/*tag= c	
FT		/note= "encodes RaAP2"	
XX			
XX			
PN	WO200011175-A1.		
PD			
PD	02-MAR-2000.		
XX			
PF	17-AUG-1999;	99WO-GB002716.	
XX			
XX	18-AUG-1998;	98GB-00018001.	
PR	04-DEC-1998;	98GB-00026753.	
XX			
PA	(ZENEC ) ZENECA LTD.		
XX			
PI	Broekaert WF, Francois IEUA, De Bolle MFC, Evans IU, Ray JA;		
XX			
DR	WPI, 2000-246564/21.		
DR	P-PsDB; AAY84058.		
PT			
PT	Improving expression of polyproteins in plants involves coexpression of		
PT	two or more proteins in plants within a single transcription unit.		
XX			
PS	Example 2; Fig 9; 151pp; English.		
CC	The present sequence encodes a protein of the invention, comprising the		
CC	mature proteins of the plant defensins, the Dahlia antimicrobial protein		
CC	(AMP) 1 and the antifungal protein 2 (APF2), linked by a linker		
CC	improving expression levels of one or more proteins in a transgenic		
CC	plant. The method comprises inserting a DNA sequence having a promoter		
CC	region operably linked to two or more protein encoding regions separated		
CC	by a DNA sequence coding for a linker propeptide and a terminator region.		
CC	The method is used to produce proteins in plants. The linker propeptide		
CC	comprising a cleavage site, whereby the expressed polyprotein is post-		
CC	translationally processed into the component protein molecules. The		
CC	propeptide sequence is rich in amino acids A, V, S and T and contains		
CC	dipeptidic sequences consisting of either two acidic, two basic or one		
CC	acidic and one basic residue as a cleavable linker sequence		
XX			
SQ	Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;		
Query Match	48.3%;	Score 215.2; DB 3; Length 534;	
Best Local Similarity	98.6%;	Pred. No. 4e-45;	
Matches 217; Conservative	0; Mismatches	3; Indels	0; Gaps 0;
QY	155 AGATATCCGATCCGTTAGTGAGAACTGTGCGAGAAAGCTAGCAAGACATGGTCGGGAAA	214	
DB	138 AGATATCCGATCCGTTAGTGAGAACTGTGCGAGAAAGCTAGCAAGACATGGTCGGGAAA	197	
OY	215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAAATCATGTGGAGGGTGGGCCCATGG	274	
DB	198 CTGTGGCAACACGGGACATTTGTGACAAACCAATGTAAATCATGTGGAGGGTGGGCCCATGG	257	
OY	275 AGCGTGATGCGCTAAACGGGAAACACATGCTTTCTGTAATCTCAATTGTAAAAAGC	334	
DB	258 AGCGTGATGCGCTAAACGGGAAACACATGCTTTCTGTAATCTCAATTGTAAAAAGC	317	
OY	335 CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGACAACTC	374	
DB	318 CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGACAACTC	357	
AAZ99335	standard; DNA; 485 BP.		
AAZ99335			
AAZ99335			
DT	03-JUL-2000 (First entry)		

Key	Location/Qualifiers
FT CDS	3..476
FT	/*tag= a
FT	/product= "fusion protein of DmAMP1 and RsaFP2"
XX	WO200011175-A1.
XX	02-MAR-2000.
XX	17-AUG-1999; 99WO-GB002716.
XX	18-AUG-1998; 98GB-00018001.
XX	04-DEC-1998; 98GB-00026753.
XX	(ZENEC ) ZENECA LTD.
XX	Broekaert WF, Francois IEJA, De Bolle MFC, Evans IU, Ray JA;
XX	WPI: 2000-246564/21.
XX	P-PSDB; AAY84068.
XX	Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
XX	Disclosure; Fig 30; 151pp; English.
XX	The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (RsaFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The CC propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
XX	Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;
XX	Query Match 47.5%; Score 212; DB 3; Length 485;
XX	Best Local Similarity 97.7%; Pred. No. 3e-48;
XX	Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	155 AGATATGCCATCCGTTAGTGGAGAACTATGGCAAGACATGTCGGGAAA 214
DB	65 AGATATGCCATCCGTTAGTGGAGAACTATGGCAAGACATGTCGGGAAA 124
QY	215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAAATCATGGAGGTCGGCCATGG 274
DB	125 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAAATCATGGAGGTCGGCCATGG 184
QY	275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAAAAAAGC 334
DB	185 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAAAAAAGC 244
QY	335 CGAAAAGCTTGCTCAAGCAAACTTAAAGCGGAACAATC 374
DB	245 CGAAAAGCTTGCTCAAGCAAACTTAAAGCGGAACAATC 284

RESULT 8  
ADM77231  
ID ADM77231 standard; cDNA; 529 BP.

AC ADM77231;

DT 03-JUN-2004 (first entry)

XX Ironweed cDNA encoding mature defensin #2.

XX Ironweed; ss; EST; expressed sequence tag; defensin;

XX soybean cyst nematode; pesticide; plant; plant pathogen;

XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.

XX Vernonia mespilifolia.

XX US2003140368-A1.

XX 24-JUL-2003.

XX 21-JUN-2002; 2002US-00178449.

XX 25-OCT-2001; 2001US-00030516.

XX (PION-) PIONEER HI-BRED INT INC.

XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK,

XX Rafalski JA, Weng Z;

XX WPI; 2003-851760/79.

XX P-PSDB; ADM77232.

XX New nucleic acid molecule, useful for preparing a composition for

XX treating fungal infections, e.g. Candidiasis.

XX Claim 1; SEQ ID NO 48; 69pp; English.

XX The invention relates to an isolated nucleic acid molecule (either an

XX EST, expressed sequence tag or an EST contig) encoding a plant defense

XX or its mature form, or the complement of them. Also included are a DNA

XX construct comprising the novel nucleic acid (operably linked to a

XX promoter that drives expression in a host cell), an expression cassette

XX comprising the DNA construct, a host cell having stably incorporated into

XX its genome the DNA construct, an isolated polypeptide and impacting a

XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The

XX nucleic acid construct is useful for preparing a composition for treating

XX fungal infections, e.g. Candidiasis. The present sequence is either an

XX EST (expressed sequence tag) or an EST contig encoding a plant defensin

XX or its mature form.

XX Sequence 529 BP; 178 A; 88 C; 111 G; 148 T; 0 U; 4 Other;

XX Query Match 47.0%; Score 209.4; DB 11; Length 529;

XX Best Local Similarity 82.5%; Pred. No. 1.6e-47;

XX Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

XX

QY 395 CCAAAAGCTTGACCGTGATGCCAGAAAGTGGTCCAAAGCTTGAAACATCC 445  
DB 318 AGATAAGTTTGACCATGATGCAGAAAGAGTAGTACCAATGTCAGAACATCC 368

RESULT 9  
ADM77214  
ID ADM77214 standard; cDNA; 579 BP.

AC ADM77214;

DT 03-JUN-2004 (first entry)

XX Ironweed cDNA encoding mature defensin #1.

XX Ironweed; ss; EST; expressed sequence tag; defensin;

XX soybean cyst nematode; pesticide; plant; plant pathogen;

XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.

XX Vernonia mespilifolia.

XX US2003140368-A1.

XX 24-JUL-2003.

XX 21-JUN-2002; 2002US-00178449.

XX 25-OCT-2001; 2001US-00030516.

XX (PION-) PIONEER HI-BRED INT INC.

XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK,

XX Rafalski JA, Weng Z;

XX WPI; 2003-851760/79.

XX P-PSDB; ADM77215.

XX New nucleic acid molecule, useful for preparing a composition for

XX treating fungal infections, e.g. Candidiasis.

XX Claim 1; SEQ ID NO 31; 69pp; English.

XX The invention relates to an isolated nucleic acid molecule (either an

XX EST, expressed sequence tag or an EST contig) encoding a plant defensin

XX or its mature form, or the complement of them. Also included are a DNA

XX construct comprising the novel nucleic acid (operably linked to a

XX promoter that drives expression in a host cell), an expression cassette

XX comprising the DNA construct, a host cell having stably incorporated into

XX its genome the DNA construct, an isolated polypeptide and impacting a

XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The

XX nucleic acid construct is useful for preparing a composition for treating

XX fungal infections, e.g. Candidiasis. The present sequence is either an

XX EST (expressed sequence tag) or an EST contig encoding a plant defensin

XX or its mature form.

XX Sequence 579 BP; 198 A; 97 C; 117 G; 167 T; 0 U; 0 Other;

XX Query Match 45.5%; Score 203; DB 11; Length 579;

XX Best Local Similarity 81.1%; Pred. No. 9.5e-46;

XX Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

XX



CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX

SO Sequence 485 BP; 124 A; 107 C; 128 G; 126 T; 0 U; 0 Other;

Query Match 38.8%; Score 173.2; DB 3; Length 485;  
 Best Local Similarity 85.1%; Pred. No. 1.5e-37;  
 Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAAGACATGTCGGGAAA 214  
 65 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAAGACATGTCGGGAAA 124  
 215 CTGTGGCAATACCGGACATTTGTGACAAACAATGTAATCATGGAGGGTCCGCTCACGG 274  
 125 CTGTGGCAATACCGGACATTTGTGACAAACAATGTAATCATGGAGGGTCCGCTCACGG 184  
 275 AGCGTGTATGTCGCTGTAACGGGAAACACATGTTTCTGTACTTCAATTGTAATAAAGC 334  
 185 AGCGTGTATGTCGCTGTAACGGGAAACACATGTTTCTGTACTTCAATTGTCGTACGC 244  
 335 CGAAAGCTTGTCTCAAGACAACTTAAG---CCGACACATGCTGCTCAAGACAACTTA 391  
 245 TGAAGAAAGCTGTGCTGCTCTTCTCTTAAGCTTCTGAAGAACTGCTCAAGAAAGCTCC 304  
 392 TG 393  
 305 TG 306

## RESULT 12

\*AAZ99329  
 ID AAZ99329 standard; DNA; 446 BP.

AAZ99329;

03-JUL-2000 (first entry)

DNA encoding a fusion protein of DmAMP1 and RsaFP2.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; ss.

Synthetic.

Dahlia merckii.

Unidentified.

Key Location/Qualifiers  
 CDS 3..437  
 /tag= a  
 /product= "fusion protein of DmAMP1 and RsaFP2"

MO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99MO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENNE ) ZENNECA LTD.

Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

WPI; 2000-246564/21.

P-PSDB; AAY84062.

Improving expression of polypeptides in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.

XX Disclosure, Fig 24, 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX

SO Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other;

Query Match 38.6%; Score 172.2; DB 3; Length 446;  
 Best Local Similarity 93.3%; Pred. No. 2.7e-37;  
 Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAAGACATGTCGGGAAA 214  
 65 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAAGACATGTCGGGAAA 124  
 215 CTGTGGCAATACCGGACATTTGTGACAAACAATGTAATCATGGAGGGTCCGCTCACGG 274  
 125 CTGTGGCAATACCGGACATTTGTGACAAACAATGTAATCATGGAGGGTCCGCTCACGG 184  
 275 AGCGTGTATGTCGCTGTAACGGGAAACACATGTTTCTGTACTTCAATTGTAATAAAGC 334  
 185 AGCGTGTATGTCGCTGTAACGGGAAACACATGTTTCTGTACTTCAATTGTAACGCGC 244  
 335 CGAAAGCTTGTCT 347  
 245 CGACGAGTGGCT 257

## RESULT 13

\*AAZ99334  
 ID AAZ99334 standard; DNA; 1093 BP.

AAZ99334;

03-JUL-2000 (first entry)

DNA encoding a fusion protein of DmAMP1, RsaFP2, HsaFP1 and AceAMP1.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; ss.

Synthetic.

Dahlia merckii.

Unidentified.

Key Location/Qualifiers  
 CDS 3..1085  
 /tag= a  
 /product= "fusion protein of plant defensins"

MO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99MO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENNE ) ZENNECA LTD.



```
XX PI Broekert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI: 2000-246564/21.
XX P-PSDB: AAY64057.
XX DR
XX PT Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX PS Disclosure, Fig 29; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX mature protein of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1, antifungal protein 2 (RAFP2), HsAFP1, and AceAMP1, linked by
XX linker propeptides of the invention. The specification describes methods
XX for improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX SQ Sequence 1093 BP; 278 A; 271 C; 287 G; 257 T; 0 U; 0 Other;
XX
XX Query Match 38.1%; Score 170; DB 3; Length 1093;
XX Best Local Similarity 84.3%; Pred. No. 1.5e-36;
XX Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
XX
XX QY 155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGCATGTCGGGAAA 214
XX |||
XX DB 65 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGCATGTCGGGAAA 124
XX
XX QY 215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGGCCCATGG 274
XX |||
XX DB 125 CTGTGGCAACACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGGCCCATGG 184
XX
XX QY 275 AGCGTGCATGTGGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
XX |||
XX DB 185 AGCGTGCATGTGGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAACTGCGCTAACGC 244
XX
XX QY 335 CGAAAAGCTTGCTCAAGACAACTTAAG---CCGAACAACCTCGCTCAAGCAAACTTAA 391
XX |||
XX DB 245 TGAGGAAGCTGCTGCTGCTATTCTGAAGCTTCTGAAGAACTTCTCAAGAAAGCTCC 304
XX
XX QY 392 TG 393
XX ||
XX DB 305 TG 306
XX
XX RESULT 14
XX AA299324 ID AA299324 standard; DNA; 522 BP.
XX XX AA299324;
XX AC
XX XX 03-JUL-2000 (first entry)
XX DT
XX XX DNA encoding a fusion protein of DmAMP1 and RAFP2.
XX DE
XX XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX KW protein expression; plant defensin; RAFP2; antifungal protein; AFP2; BS.
XX XX
XX OS Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX XX
XX FH Key Location/Qualifiers
XX misc_feature 160..309
XX FT /*tag= a
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FT FT /note= "encodes DmAMP1"
FT FT misc_feature 358..510
FT FT /*tag= b
FT FT /note= "encodes RAFP2"
XX XX
XX XX W0200011175-A1.
XX XX
XX XX 02-MAR-2000.
XX XX
XX XX 17-AUG-1999; 99WC-GB002716.
XX XX
XX XX 18-AUG-1998; 98GB-00018001.
XX XX
XX XX 04-DEC-1998; 98GB-00026753.
XX XX
XX XX (ZENEC) ZENEC LTD.
XX XX
XX PI Broekert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI: 2000-246564/21.
XX DR P-PSDB: AAY64057.
XX XX
XX XX Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 8; 151pp; English.
XX
XX CC The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
XX
XX Query Match 37.9%; Score 169.2; DB 3; Length 522;
XX Best Local Similarity 95.6%; Pred. No. 1.9e-36;
XX Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGCATGTCGGGAAA 214
XX |||
XX DB 138 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGCATGTCGGGCAA 197
XX
XX QY 215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGGCCCATGG 274
XX |||
XX DB 198 CTGTGGCAACACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGGCCCATGG 257
XX
XX QY 275 AGCGTGCATGTGGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
XX |||
XX DB 258 AGCGTGCATGTGGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTCCAAAGC 317
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XX QY 335 CG 336
XX ||
XX DB 318 TG 319
XX
XX RESULT 15
XX AA54387 ID AA54387 standard; DNA; 460 BP.
XX XX AA54387;
XX AC
XX XX AA54387;
XX DT
XX XX 11-APR-2001 (first entry)
XX DE plant defensin coding sequence.
```





Query Match 100.0%; Score 446; DB 6; Length 446;  
Best Local Similarity 100.0%; Pred. No. 7.4e-105;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGGATCGGTCGGTCCGCTTCGCTTCGATCCCTTTCGCTCCATC 60  
DB 1 ATGGGATCGGTCGGTCCGCTTCGCTTCGATCCCTTTCGCTCCATC 60  
OY 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATAGATTTATTTATG 120  
DB 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATAGATTTATTTATG 120  
OY 121 TTTTATGTTCTGCAAGTTGCAAAATTTAGTATGATATGATCCGTTAGTGA 180  
DB 121 TTTTATGTTCTGCAAGTTGCAAAATTTAGTATGATATGATCCGTTAGTGA 180  
OY 181 TATCGGAAAGCTAGCAAGCATGTGCGGAACTGTGGCAATACGGGACATTGTGACA 240  
DB 181 TATCGGAAAGCTAGCAAGCATGTGCGGAACTGTGGCAATACGGGACATTGTGACA 240  
OY 241 ACCAATGTAATCATGGAGGGTGGCCCATGAGCGTGCATGTGCTTAACGGGAAAC 300  
DB 241 ACCAATGTAATCATGGAGGGTGGCCCATGAGCGTGCATGTGCTTAACGGGAAAC 300  
OY 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGCTCAAGCAAACTTA 360  
DB 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGCTCAAGCAAACTTA 360  
OY 361 AAGCCGAACAACCTGCTCAAGCAAACTTAATGCCCCAAGCTTGACCGTGAACCAAGA 420  
DB 361 AAGCCGAACAACCTGCTCAAGCAAACTTAATGCCCCAAGCTTGACCGTGAACCAAGA 420  
OY 421 AAGTGTTCCAAACGTTGAACATCCG 446  
DB 421 AAGTGTTCCAAACGTTGAACATCCG 446

RESULT 2  
BD240919 446 bp DNA linear PAT 17-JUL-2003  
LOCUS Polynucleotide sequences.  
DEFINITION BD240919.1 GI:33050689  
ACCESSION BD240919.1 GI:33050689  
VERSION  
KEYWORDS JP 2002523052-A/5.  
SOURCE Dahlia merckii (bedding dahlia)  
ORGANISM Dahlia merckii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Cisteoideae; Dahlia.  
REFERENCE 1 (bases 1 to 446)  
AUTHORS Evans, I.J. and Ray, J.A.  
TITLE Polynucleotide sequences  
JOURNAL Patent: JP 2002523052-A 5 30-JUL-2002;  
SYNGENTA LTD  
COMMENT OS Dahlia merckii (dahlia)  
PN JP 2002523052-A/5  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566448  
PR 18-AUG-1998 GB 9818003.7  
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY  
PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//C12N5/10,C12R1:91),  
PC C12N15/00,  
CC C12N5/00,(C12N5/00,C12R1:91)  
CDS Polynucleotide sequences  
FH Key Location/Qualifiers  
FT CDS (1)..(64).  
Location/Qualifiers  
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/organism="Dahlia merckii"  
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ORIGIN  
Query Match 100.0%; Score 446; DB 6; Length 446;  
Best Local Similarity 100.0%; Pred. No. 7.4e-105;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGAATCGGTCGGTTCGCTTCGCGCTTCTGATCCCTTTCGCTCCATC 60  
DB 1 ATGGTGAATCGGTCGGTTCGCTTCGCGCTTCTGATCCCTTTCGCTCCATC 60  
OY 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATAGATTTATTTATG 120  
DB 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATAGATTTATTTATG 120  
OY 121 TTTTATGTTCTGCAAGTTGCAAAATTTAGATAGATATGATCCGTTAGTGA 180  
DB 121 TTTTATGTTCTGCAAGTTGCAAAATTTAGATAGATATGATCCGTTAGTGA 180  
OY 181 TATCGGAAAGCTAGCAAGCATGTGCGGAACTGTGGCAATACGGGACATTGTGACA 240  
DB 181 TATCGGAAAGCTAGCAAGCATGTGCGGAACTGTGGCAATACGGGACATTGTGACA 240  
OY 241 ACCAATGTAATCATGGAGGGTGGCCCATGAGCGTGCATGTGCTTAACGGGAAAC 300  
DB 241 ACCAATGTAATCATGGAGGGTGGCCCATGAGCGTGCATGTGCTTAACGGGAAAC 300  
OY 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGCTCAAGCAAACTTA 360  
DB 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGCTCAAGCAAACTTA 360  
OY 361 AAGCCGAACAACCTGCTCAAGCAAACTTAATGCCCCAAGCTTGACCGTGAACCAAGA 420  
DB 361 AAGCCGAACAACCTGCTCAAGCAAACTTAATGCCCCAAGCTTGACCGTGAACCAAGA 420  
OY 421 AAGTGTTCCAAACGTTGAACATCCG 446  
DB 421 AAGTGTTCCAAACGTTGAACATCCG 446

RESULT 3  
BD223236 606 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.  
DEFINITION BD223236  
ACCESSION BD223236  
VERSION BD223236.1 GI:33033006  
KEYWORDS JP 2002523047-A/5.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 606)  
AUTHORS Broekert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polypeptide in plant  
JOURNAL Patent: JP 2002523047-A 5 30-JUL-2002;  
SYNGENTA LTD  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/5  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI  
PI WILLEM FRANS BROEKERT, ISABELLE ELSA JEANNE  
PI AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN ANTHONY RAY  
PC C12N15/09,A01H1/00,C07K12,C12N5/10,C12P21/02//C12N5/10,PC  
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
CDS Location/Qualifiers  
FT CDS (76)..(597).  
Location/Qualifiers  
1..606  
/organism="synthetic construct"

/mol\_type="genomic DNA"  
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ORIGIN

Query Match 64.4%; Score 287.2; DB 6; Length 606;  
Best Local Similarity 99.0%; Pred. No. 1.1e-63;  
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197  
QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 317

QY 335 CGAAAAGCTTGCTCTCAAGCAAACTTAAAGCCGAACATCGCTCAAGCAAACTTAATGC 394  
DB 318 CGAAAAGCTTGCTCTCAAGCAAACTTAAAGCCGAACATCGCTCAAGCAAACTTAATGC 377

QY 395 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 446  
DB 378 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 429

RESULT 4  
BD223246 557 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polyprotein in plant.  
DEFINITION BD223246  
ACCESSION BD223246 GI:33033016  
VERSION JP 2002523047-A/15.  
KEYWORDS JP 2002523047-A/15.  
SOURCE  
ORGANISM  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 557)  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polyprotein in plant  
JOURNAL Patent: JP 2002523047-A 15 30-JUL-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/15  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91,  
CC C12N15/00, C12N5/00, C12N5/00, C12R1:91  
CDS Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers  
FT CDS Location/Qualifiers

FEATURES  
source  
1..557  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 63.7%; Score 284; DB 6; Length 557;  
Best Local Similarity 98.3%; Pred. No. 7.6e-63;  
Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197  
QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 317

DB 65 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 124  
QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 125 CTGTGGCAACACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 184  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 334  
DB 185 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 244

QY 335 CGAAAAGCTTGCTCTCAAGCAAACTTAAAGCCGAACATCGCTCAAGCAAACTTAATGC 394  
DB 245 CGAAAAGCTTGCTCTCAAGCAAACTTAAAGCCGAACATCGCTCAAGCAAACTTAATGC 304

QY 395 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 446  
DB 305 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 356

RESULT 5  
BD223234 534 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polyprotein in plant.  
DEFINITION BD223234  
ACCESSION BD223234 GI:33033004  
VERSION JP 2002523047-A/3.  
KEYWORDS JP 2002523047-A/3.  
SOURCE  
ORGANISM  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polyprotein in plant  
JOURNAL Patent: JP 2002523047-A 3 30-JUL-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/3  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91,  
CC C12N15/00, C12N5/00, C12N5/00, C12R1:91  
CDS Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers  
FT CDS Location/Qualifiers

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source  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 48.3%; Score 215.2; DB 6; Length 534;  
Best Local Similarity 98.6%; Pred. No. 5.2e-45;  
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197  
QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACATGTGTTCTGTTACTTCAATTGTAATAAAGC 317

QY	335	CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGAAACAATC	374
Db	318	CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGAAACAATC	357
RESULT 6			
LOCUS	BD240936	534 bp	DNA
DEFINITION	Polynucleotide sequences.		
ACCESSION	BD240936		
VERSION	BD240936.1	GI:33050706	
KEYWORDS	JP 2002523052-A/22.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	Other sequences; artificial sequences.		
AUTHORS	1 (bases 1 to 534)		
TITLE	Evans, I.J. and Ray, J.A.		
JOURNAL	Polynucleotide sequences		
	Patent: JP 2002523052-A 22 30-JUL-2002;		
	SYNGENTA LTD		
COMMENT	OS Artificial Sequence		
	PN JP 2002523052-A/22		
	PD 30-JUL-2002		
	PF 17-AUG-1999 JP 2000566448		
	PR 18-AUG-1998 GB 9818003.7		
	PI IAN JEFFREY EVANS, JOHN ANTHONY RAY		
	PC C12N15/09, A01H5/00, C07K14/415, C12N5/10//C12N5/10, C12R1:911,		
	PC C12N5/00, C12N5/00, C12R1:911		
	PC C12N5/00, C12N5/00, C12R1:911		
	CC Description of Artificial Sequence: Synthetic sequence FH		
Key	Location/Qualifiers		
FT	CDS (76)..(525).		
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Source	1..534		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
ORIGIN			
Query Match	48.3%; Score 215.2; DB 6; Length 534;		
Best Local Similarity	98.6%; Pred. No. 5.2e-45;		
Matches 217; Conservative	0; Mismatches 3; Indels 0; Gaps 0;		
QY	155	AGATATGCCATTCGTTAGTGGAGAACTATGCGAAGCTAGCAAGACATGTCGGGAAA	214
Db	138	AGATATCCCATCCGTTAGTGGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGCAA	197
QY	215	CTGTGGCAATACGGGACATTTGGACAAACAATGTAAATCATGGGAGGGTGGCCCATGG	274
Db	198	CTGTGGCAACACGGGACATTTGGACAAACAATGTAAATCATGGGAGGGTGGCCCATGG	257
QY	275	AGCGTGTATGTCGTAAACGGGAAACACATGTGTTTCTGTTACTTCATTGTAAGAAAAGC	334
Db	258	AGCGTGTATGTCGTAAACGGGAAACACATGTGTTTCTGTTACTTCATTGTAAGAAAAGC	317
QY	335	CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGAAACAATC	374
Db	318	CGAAAAGCTTGCTCAAGACAAACTTAAAGCCGAAACAATC	357
RESULT 7			
LOCUS	BD223245	485 bp	DNA
DEFINITION	Method of genetic expression of polyprotein in plant.		
ACCESSION	BD223245		
VERSION	BD223245.1	GI:33033015	
KEYWORDS	JP 2002523047-A/14.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	Other sequences; artificial sequences.		
AUTHORS	1 (bases 1 to 485)		
	Broekert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and		
	Ray, J.A.		

TITLE	Method of genetic expression of polyprotein in plant									
JOURNAL	Patent: JP 2002523047-A 14 30-JUL-2002;									
COMMENT	SYNGENTA LTD OS Artificial Sequence PN JP 2002523047-A/14 PD 30-JUL-2002 PF 17-AUG-1999 JP 2000566429 PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI WILLEM FRANS BROEKHART, ISABELLE ELSA JEANNE AUGUSTINE FRANCOIS, PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P2/02, (C12N5/10, PC C12R1:91), PC C12N15/00, C12N5/00, C12R1:91) CC Description of Artificial Sequence: Synthetic sequence FH Key Location/Qualifiers FT CDS (3)..(476).									
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Query Match	47.5%; Score 212; DB 6; Length 485;									
Best Local Similarity	97.7%; Pstd. No. 3.5e-44;									
Matches 215; Conservative	0; Mismatches 5; Indels 0; Gaps 0;									
OY	155 AGATATGCGATCCGTTAGTGGAGAACATATCGAGAAAGTACGACATGTCGGGAAA 214									
Db	65 AGATATGCGATCCGTTAGTGGAGAACATATCGAGAAAGTACGACATGTCGGGAAA 124									
OY	215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTCGGCCCATGG 274									
Db	125 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTCGGCCCATGG 184									
OY	275 AGCGTGTCAATGTGCGTAAACGGGAAACATATGTTTCTGTACTTCAATTGTAAAAAGC 334									
Db	185 AGCGTGTCAATGTGCGTAAACGGGAAACATATGTTTCTGTACTTCAATTGTAAAAAGC 244									
OY	335 CGAAAGCTTGCTCAAGACAAACTTAAAGCGGAAACAATC 374									
Db	245 CGAAAGCTTGCTCAAGACAAACTTAAAGCGGAAACAATC 284									
RESULT 8										
BD240918										
LOCUS	BD240918 577 bp DNA linear PAT 17-JUL-2003									
DEFINITION	Polynucleotide sequences.									
ACCESSION	BD240918									
VERSION	BD240918.1 GI:33050688									
KEYWORDS	JP 2002523052-A/4.									
SOURCE	Dahlia merckii (bedding dahlia)									
ORGANISM	Dahlia merckii Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsideae; Dahlia. 1 (bases 1 to 577).									
REFERENCE	1. (bases 1 to 577).									
AUTHORS	Evans,I.J. and Ray,J.A.									
TITLE	Polynucleotide sequences									
JOURNAL	Patent: JP 2002523052-A 4 30-JUL-2002;									
COMMENT	SYNGENTA LTD OS Dahlia merckii (dahlia) PN JP 2002523052-A/4 PD 30-JUL-2002 PF 17-AUG-1999 JP 2000566448 PR 18-AUG-1998 GB 9818003.7 PI IAN JEFFREY EVANS, JOHN ANTHONY RAY PC C12N15/09, A01H5/00, C07K1/415, C12N5/10, (C12N5/10, C12R1:91), PC C12N15/00, PC C12N5/00, (C12N5/00, C12R1:91)									

CC Polynucleotide sequences  
FH Key Location/Qualifiers  
FT CDS (20)..(346).  
FEATURES  
SOURCE Location/Qualifiers  
1..577  
/organism="Dahlia merckii"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:43367"

## ORIGIN

Query Match 39.7%; Score 177.2; DB 6; Length 577;  
Best Local Similarity 80.1%; Pred. No. 3.7e-35;  
Matches 234; Conservative 0; Mismatches 28; Indels 30; Gaps 1;

OY 155 AGATATGCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
|||  
DB 82 AGATATCCAGAGTGAAGAGAGAGATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 141  
|||  
OY 215 CTGTGGCAATACGGGACATTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
|||  
DB 142 CTGTGGCAATACGGGACATTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 201  
|||  
OY 275 AGCGTGTATGTGCGTAAACGGGAAACATGTTCTTCTTACTTCAATTGTAATAAAC 334  
|||  
DB 202 GCGGTGCCACGTGCGTGAAGGAAACACATGTTCTTCTTCAATTGTTCCCAAGC 261  
|||  
OY 335 CGAAAAGCTTGCTCAAGCAAACTTAAGCCGAAACAATCGCTCAAGCAAACTTAATGC 394  
|||  
DB 262 CGAAAAGCTT-----GCTCAAGCAAACTTAATGC 291  
|||  
OY 395 CGAAAAGCTTGACCGTGAAGCAAAAGTGTTCAAACGTTGAACATCCG 446  
|||  
DB 292 CCAAGAGCTTGACCGTGAAGCAAAAGTGTTCGAACGTTGAACATCCG 343  
|||

RESULT 9  
BD223243 485 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.  
DEFINITION BD223243  
ACCESSION BD223243  
VERSION BD223243.1 GI:33033013  
KEYWORDS JP 2002523047-A/12.  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
1 (bases 1 to 485)  
Method of genetic expression of polypeptide in plant

TITLE  
JOURNAL Patent: JP 2002523047-A 12 30-JUL-2002;  
SYNGENTA LTD

COMMENT  
OS Artificial Sequence  
PN JP 2002523047-A/12  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
PI WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91),  
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS (3)..(476).  
Location/Qualifiers  
1..485  
/organism="synthetic construct"  
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## FEATURES

source

## ORIGIN

Query Match 38.8%; Score 173.2; DB 6; Length 485;  
Best Local Similarity 85.1%; Pred. No. 4e-34;  
Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

OY 155 AGATATGCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
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DB 65 AGATATGCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGGAAA 124  
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OY 215 CTGTGGCAATACGGGACATTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
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DB 125 CTGTGGCAATACGGGACATTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 184  
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OY 275 AGCGTGTATGTGCGTAAACGGGAAACATGTTCTTCTTACTTCAATTGTAATAAAC 334  
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DB 185 AGCGTGTATGTGCGTAAACGGGAAACATGTTCTTCTTACTTCAATTGTTGCTAAC 244  
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OY 335 CGAAAAGCTTGCTCAAGCAAACTTAAG---CGAACATCGCTCAAGCAAACTTA 391  
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DB 245 TGAGAGAGCTGCTGCTGCTATTCCTGAAGCTTGAAGAACTGCTCAAGAAAGCTCC 304  
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OY 392 TG 393  
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DB 305 TG 306  
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RESULT 10  
BD223239 446 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.  
DEFINITION BD223239  
ACCESSION BD223239  
VERSION BD223239.1 GI:33033009  
KEYWORDS JP 2002523047-A/8.  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
1 (bases 1 to 446)  
Method of genetic expression of polypeptide in plant

TITLE  
JOURNAL Patent: JP 2002523047-A 8 30-JUL-2002;  
SYNGENTA LTD

COMMENT  
OS Artificial Sequence  
PN JP 2002523047-A/8  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
PI WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91),  
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS (3)..(437).  
Location/Qualifiers  
1..446  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## FEATURES

source

## ORIGIN

Query Match 38.6%; Score 172.2; DB 6; Length 446;  
Best Local Similarity 93.3%; Pred. No. 7.3e-34;  
Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 65 AGATATGCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGGAAA 124  
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OY 215 CTGTGGCAATACGGGACATTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
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REFERENCE 1  
AUTHORS Miao, G.H., Weng, Z. and Famodu, O. O.  
TITLE Plant defensins  
JOURNAL Patent: WO 0068405-A 3 16-NOV-2000;  
E.I. DU PONT DE NEMOURS AND COMPANY (US)  
FEATURES  
SOURCE Location/Qualifiers  
1. .460  
/organism="Dimorphotheca sinuata"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:112408"  
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Query Match 37.8%; Score 168.6; DB 6; Length 460;  
Best Local Similarity 81.6%; Pred. No. 6.3e-33;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGCTGCAAGACATGTGGGAAA 214  
Db 87 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGCTGCAAGACATGTGGGCAA 146  
Qy 215 CTGTGGCAATACGGGACATTGTGACAAACCAATGTAATCATGAGAGGGTGGCCCATGG 274  
Db 147 CTGTGGCAACCGGACACTGTGACGACAGTGTGAGTGTGGAGACTGCAAGCCCATGG 206  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 334  
Db 207 TGCCTGTATGTGGGTGGGAAACACATGTGCTTGTCTACTTCAATTGTAAAAAGC 266  
Qy 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAACACTGCTCTCAAGCAAACTTAATG 393  
Db 267 CGAAAGCTTGTCCCAAGCAAGCTCAACGCTGAAAAAATTCGGCCGTATGACGTTAAAG 325  
RESULT 14  
AX046743 503 bp DNA linear PAT 15-DEC-2000  
LOCUS Sequence 1 from Patent WO0068405.  
AX046743  
AX046743.1 GI:11876280  
VERSION  
KEYWORDS Dimorphotheca sinuata (African daisy)  
SOURCE Dimorphotheca sinuata  
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Calenduleae; Dimorphotheca.  
REFERENCE 1  
AUTHORS Miao, G.H., Weng, Z. and Famodu, O. O.  
TITLE Plant defensins  
JOURNAL Patent: WO 0068405-A 1 16-NOV-2000;  
E.I. DU PONT DE NEMOURS AND COMPANY (US)  
FEATURES  
SOURCE Location/Qualifiers  
1. .503  
/organism="Dimorphotheca sinuata"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 37.8%; Score 168.6; DB 6; Length 503;  
Best Local Similarity 81.6%; Pred. No. 6.3e-33;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGCTGCAAGACATGTGGGAAA 214  
Db 80 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGCTGCAAGACATGTGGGCAA 139

Qy 215 CTGTGGCAATACGGGACATTGTGACAAACCAATGTAATCATGAGAGGGTGGCCCATGG 274  
Db 140 CTGTGGCAACCGGACACTGTGACGACGAGTGTGAGTGTGGAGACTGCAAGCCCATGG 199  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 334  
Db 200 TGCCTGTATGTGGGTGGGAAACACATGTGCTTGTCTACTTCAATTGTAAAAAGC 259  
Qy 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAACACTGCTCTCAAGCAAACTTAATG 393  
Db 260 CGAAAGCTTGTCCCAAGCAAGCTCAACGCTGAAAAAATTCGGCCGTATGACGTTAAAG 318  
RESULT 15  
BD223237 534 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.  
BD223237  
BD223237.1 GI:33033007  
VERSION  
KEYWORDS JP 2002523047-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Broekert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polypeptide in plant  
JOURNAL Patent: JP 2002523047-A 6 30-JUL-2002;  
SYNGENTA LTD  
OS Artificial Sequence  
PN JP 2002523047-A/6  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI  
WULLEN FRANS BROEKERT, ISABELLE ELSA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC  
C12R1:91),  
PC C12N15/00, C12N5/00, C12N5/00, C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers  
1. .534  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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Query Match 37.5%; Score 167.2; DB 6; Length 534;  
Best Local Similarity 98.3%; Pred. No. 1.5e-32;  
Matches 169; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGCTGCAAGACATGTGGGAAA 214  
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Qy 215 CTGTGGCAATACGGGACATTGTGACAAACCAATGTAATCATGAGAGGGTGGCCCATGG 274  
Db 198 CTGTGGCAACCGGACACTGTGACGACAGTGTGAGTGTGGAGACTGCAAGCCCATGG 257  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGT 326  
Db 258 AGCGTGTATGTGGGTGGGAAACACATGTGCTTGTCTACTTCAATTGT 309  
Search completed: March 18, 2005, 14:31:02  
Job time : 2320 secs

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RESULT 2  
US-08-377-687-31  
Sequence 31, Application US/08377687  
Patent No. 5516525  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-377-687-31

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAATATGCGAAGAACTAGACAGACATGTCGGGAAACTGTGGCAATAGCGGACATTGT 236  
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QY 237 GACACCAATGTAAATCATGAGAGGTGCGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATPACCAATGCAAGCTTGGGAGGAGCTGCTCATGAGACTTGCATGTAAAGACGA 120

QY 297 AAACACATGTGTTCTTCTTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

*is there seq idb*

RESULT 3  
US-08-777-192-31  
Sequence 31, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-777-192-31

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAATATGCGAAGAACTAGACAGACATGTCGGGAAACTGTGGCAATAGCGGACATTGT 236  
DB 1 GACCTTTGCGAAGAGCTTCTTAAGACTTGTCTGGAACACGCGAAACACTGGACATTGC 60

QY 237 GACACCAATGTAAATCATGAGAGGTGCGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATPACCAATGCAAGCTTGGGAGGAGCTGCTCATGAGACTTGCATGTAAAGACGA 120

QY 297 AAACACATGTGTTCTTCTTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 4  
US-08-971-982-31  
Sequence 31, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-No. 6187904-1597  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-08-971-982-31

Query Match 22.3%; Score 99.4; DB 3; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4,66-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGCATATACGGGCAATTGT 236  
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QY 237 GACACCAATGTAATCATGAGAGGTCGCGCCCATGAGCGTCTCATGTGCGTAACGGG 296  
DB 61 GATACCAATGCAAGTCTTGAGAGGAGCTGCTCATGAGCTTCCATGTAGAAACGA 120

QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGCTACTTCACTG 149

RESULT 5  
US-08-377-687-33  
Sequence 33, Application US/08377687  
Patent No. 5538525

GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
US-08-377-687-33

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
US-08-377-687-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGCATATACGGGCAATTGT 236  
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QY 237 GACACCAATGTAATCATGAGAGGTCGCGCCCATGAGCGTCTCATGTGCGTAACGGG 296  
DB 61 GATACCAATGCAAGTCTTGAGAGGAGCTGCTCATGAGCTTCCATGTAGAAACGA 120

QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGCTACTTCACTG 149

RESULT 6  
US-08-777-192-33  
Sequence 33, Application US/08777192  
Patent No. 5824869

GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
US-08-377-687-33

not instant  
seq ID 6

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGCGAAAGTGTGCAATACGGGCAATTGT 236  
DB 1 GAGCTTGGCAGAAAGCTTCTTAAGACTTGTCTGGAAGCTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAAATCATGAGAGGTGCGGCCCATGAGCCGTGTGTCATGTGCGTAACGGG 236  
DB 61 GATGATCAATGCAAGCTTGGGAGGAGCTGCTCATGAGCTTGCATGTAGAAACGGA 120  
QY 297 AACACATGTGTTCTTCTTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTTCTTCACTG 149

RESULT 7  
US-08-971-982-33  
Sequence 33, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
CAMMUE, BRUNO P.A.  
OSBORN, RUPERT W.  
REES, SARAH B.  
TERRAS, FRANKY R.G.  
VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-No. 6187904-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-971-982-33

Query Match 20.5%; Score 91.4; DB 3; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGCGAAAGTGTGCAATACGGGCAATTGT 236  
DB 1 GAGCTTGGCAGAAAGCTTCTTAAGACTTGTCTGGAAGCTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAAATCATGAGAGGTGCGGCCCATGAGCCGTGTGTCATGTGCGTAACGGG 236  
DB 61 GATGATCAATGCAAGCTTGGGAGGAGCTGCTCATGAGCTTGCATGTAGAAACGGA 120  
QY 297 AACACATGTGTTCTTCTTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTTCTTCACTG 149

RESULT 8  
US-08-377-687-34  
Sequence 34, Application US/08377687  
Patent No. 5538525  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
CAMMUE, BRUNO P.A.  
OSBORN, RUPERT W.  
REES, SARAH B.  
TERRAS, FRANKY R.G.  
VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-377-687-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTGGCGAAGAGGCTTTAAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGGAGGGTGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATAACAAGTGCAAGTCTTGGAGGAGGAGCTGCTCATGAGCGTTCATGTAAGATCTTGA 120  
QY 297 AAACACATGTTCTTCTGTTACTTCAATG 325  
DB 121 AAGCATATGCTTCTGCTACTTCAATG 149

## RESULT 9

US-08-777-192-34  
Sequence 34, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777.192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002.480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16.773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTGGCGAAGAGGCTTTAAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGGAGGGTGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATAACAAGTGCAAGTCTTGGAGGAGGAGCTGCTCATGAGCGTTCATGTAAGATCTTGA 120  
QY 297 AAACACATGTTCTTCTGTTACTTCAATG 325  
DB 121 AAGCATATGCTTCTGCTACTTCAATG 149

## RESULT 10

US-08-971-982-34  
Sequence 34, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971.982  
FILING DATE: 17-NOV-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002.480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16.773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-08-971-982-34

Query Match 19.4%; Score 86.6; DB 3; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTGGCGAAGAGGCTTTAAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGGAGGGTGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATAACAAGTGCAAGTCTTGGAGGAGGAGCTGCTCATGAGCGTTCATGTAAGATCTTGA 120

QY 297 AACACATGCTTCTGTTACTTCAATTG 325  
Db 121 AACGATATGCTTCTGTTACTTCAATTG 149

## RESULT 11

US-08-377-687-36  
Sequence 36, Application US/08377687  
Patent No. 5538525  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, ROBERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-377-687-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 178 AACTATCGAGAAAGCTAGCAAGCATGTGGGAAACTGTGCAATACGGGACATTGTG 237  
Db 2 ACCTTGCGAGAGAGCTTCTTACTTGACTGAACTGGAACTGGGAAACACTGGACATTGCG 61  
QY 238 ACAACCAATGTAAATCATGGAGGGTGGCCCATGAGCGTGTCTATGTGCGTAACGGGA 297  
Db 62 ATACTCATGTGCAAGAACTGGAGGCTGCTAGACATGAGGCTTGGCATTAAG---AGAGGAA 118  
QY 298 AACCATGTGTTTCTGTTACTTCAATTG 325  
Db 119 ACTGGAAGTCTTCTGTTACTTCAATTG 146

RESULT 12  
US-08-777-192-36

Sequence 36, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, ROBERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 178 AACTATCGAGAAAGCTAGCAAGCATGTGGGAAACTGTGCAATACGGGACATTGTG 237  
Db 2 ACCTTGCGAGAGAGCTTCTTACTTGACTGAACTGGAAACACTGGACATTGCG 61  
QY 238 ACAACCAATGTAAATCATGGAGGGTGGCCCATGAGCGTGTCTATGTGCGTAACGGGA 297  
Db 62 ATACTCATGTGCAAGAACTGGAGGCTGCTAGACATGAGGCTTGGCATTAAG---AGAGGAA 118  
QY 298 AACCATGTGTTTCTGTTACTTCAATTG 325  
Db 119 ACTGGAAGTCTTCTGTTACTTCAATTG 146

RESULT 13  
US-08-971-982-36  
Sequence 36, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, ROBERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.



VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-NO. 6187904-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-08-971-982-36  
Query Match 13.1%; Score 58.4; DB 3; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
QY 178 AACTATGAGAGAACTAGCAAGCATGTCGGGAACTGTGCAATACGGACATTGTG 237  
DB 2 ACCTTGGAGAGAGCTTCTTACTTGACTGGAACTGGGAACTGGACATTGCG 61  
QY 238 ACAACCAATGTAATCATGAGGAGTGGCGCCCATGAGCGTGTCTATGTCGTTAACGGGA 297  
DB 62 ATACTCAATGAGAACTGGGAGCTGCTAAGCATGAGGCTTGCCATTAAG---AGAGGAA 118  
QY 298 AACCATGTCTTCTGTTACTTCAATTG 325  
DB 119 ACTGGAAGTCTTCTGCTACTTGCATTG 146  
RESULT 14  
US-08-627-706-14  
Sequence 14, Application US/08627706  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Village Parkway No. 5773696ch  
CITY: St. Louis  
STATE: Missouri

COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,706  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-627-706-14  
Query Match 10.0%; Score 44.6; DB 1; Length 270;  
Best Local Similarity 53.8%; Pred. No. 0.00065;  
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
QY 163 CATCCGTTATGAGACTATGACGAGAACTAGCAAGATGTCGGGAACTGTGCA 222  
DB 95 CAATGTCATGATGCAAGTTGTGCGAGAGCAACCACTGGACATGTCAGAGCTTGTGGA 154  
QY 223 ATACGGACATGTGTGACACCAATGTAATCATGAGGAGTGGCGCCCATGAGACGTTGC 282  
DB 155 ACAACATGATGAGAGAGCAACCAATGCAAACTTGAAGAGCAGAACACGATCTTGCA 214  
QY 283 ATGTCGCTAACGGGAAACATATGCTTCTTACTTCAATTGTAATAAAG 333  
DB 215 ACTATGTTCTCCAGCTCACAAATGTAATGTTACTTCCATGTTAATAAG 265  
RESULT 15  
US-09-103-489-14  
Sequence 14, Application US/09103489  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Village Parkway No. 6215048ch  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-14

Query Match 10.0%; Score 44.6; DB 3; Length 270;  
Best Local Similarity 53.8%; Pred. No. 0.00065;  
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY	163	CATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCA	222
Db	95	CAATGCTGATGCAAGCTTGTGCGAGAGACCAAGTGGACATGGTCAGAGTTGTGGGA	154
QY	223	ATAGCGGACATGTGAGAACCAATGTAATCATGCGAGGTCGCCCATGAGCGTTC	282
Db	155	ACAACAATGCATGACAGAACCAATGCAGAAACCTTGAAAGACGAAACACGATCTTGCA	214
QY	283	ATGTCGTAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAATAAG	333
Db	215	ACTATGCTCTCCAGCTCACAAATGTATTTGTTACTTCCCATGTTAATAAG	265

Search completed: March 18, 2005, 16:31:56  
Job time : 137 secs